

Suzanne B

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: de la Monte, Suzanne
Wands, Jack R.

(ii) TITLE OF INVENTION: Transgenic Animals and Cell Lines for
Screening Drugs Effective for the Treatment or Prevention
of Alzheimer's Disease

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
(B) STREET: 1100 New York Ave., Suite 600
(C) CITY: Washington
(D) STATE: DC
(E) COUNTRY: USA
(F) ZIP: 20005-3934

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Esmond, Robert W.
(B) REGISTRATION NUMBER: 32,893
(C) REFERENCE/DOCKET NUMBER: 0609.4370000

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1442 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 15..1139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTTTTTTTGAG ATG GAG TTT TCG CTC TTG TTG CCC AGG CTG GAG TGC
Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys
1 5 10

AAT GGC GCA ATC TCA GCT CAC CGC AAC CTC CGC CTC CCG GGT TCA AGC Asn Gly Ala Ile Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser 15 20 25	98
GAT TCT CCT GCC TCA GCC TCC CCA GTA GCT GGG ATT ACA GGC ATG TGC Asp Ser Pro Ala Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys 30 35 40	146
ACC CAC GCT CGG CTA ATT TTG TAT TTT TTA GTA GAG ATG GAG TTT Thr His Ala Arg Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe 45 50 55 60	194
CTC CAT GTT GGT CAG GCT GGT CTC GAA CTC CCG ACC TCA GAT GAT CCC Leu His Val Gly Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro 65 70 75	242
TCC GTC TCG GCC TCC CAA AGT GCT AGA TAC AGG ACT GGC CAC CAT GCC Ser Val Ser Ala Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala 80 85 90	290
CGG CTC TGC CTG GCT AAT TTT TGT GGT AGA AAC AGG GTT TCA CTG ATG Arg Leu Cys Leu Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met 95 100 105	338
TGC CCA AGC TGG TCT CCT GAG CTC AAG CAG TCC ACC TGC CTC AGC CTC Cys Pro Ser Trp Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu 110 115 120	386
CCA AAG TGC TGG GAT TAC AGG CGT GCA GCC GTG CCT GGC CTT TTT ATT Pro Lys Cys Trp Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile 125 130 135 140	434
TTA TTT TTT TTA AGA CAC AGG TGT CCC ACT CTT ACC CAG GAT GAA GTG Leu Phe Leu Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val 145 150 155	482
CAG TGG TGT GAT CAC AGC TCA CTG CAG CCT TCA ACT CCT GAG ATC AAG Gln Trp Cys Asp His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys 160 165 170	530
CAT CCT CCT GCC TCA GCC TCC CAA GTA GCT GGG ACC AAA GAC ATG CAC His Pro Pro Ala Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His 175 180 185	578
CAC TAC ACC TGG CTA ATT TTT ATT TTT ATT TTT AAT TTT TTG AGA CAG His Tyr Thr Trp Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln 190 195 200	626
AGT CTC AAC TCT GTC ACC CAG GCT GGA GTG CAG TGG CGC AAT CTT GGC Ser Leu Asn Ser Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly 205 210 215 220	674
TCA CTG CAA CCT CTG CCT CCC GGG TTC AAG TTA TTC TCC TGC CCC AGC Ser Leu Gln Pro Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser 225 230 235	722
CTC CTG AGT AGC TGG GAC TAC AGG CGC CCA CCA CGC CTA GCT AAT TTT Leu Leu Ser Ser Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe 240 245 250	770
TTT GTA TTT TTA GTA GAG ATG GGG TTC ACC ATG TTC GCC AGG TTG ATC Phe Val Phe Leu Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile 255 260 265	818
TTG ATC TCT GGA CCT TGT GAT CTG CCT GCC TCG GCC TCC CAA AGT GCT	866

Leu Ile Ser Gly Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala			
270	275	280	
GGG ATT ACA GGC GTG AGC CAC CAC GCC CGG CTT ATT TTT AAT TTT TGT			914
Gly Ile Thr Gly Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys			
285	290	295	300
TTG TTT GAA ATG GAA TCT CAC TCT GTT ACC CAG GCT GGA GTG CAA TGG			962
Leu Phe Glu Met Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp			
305	310	315	
CCA AAT CTC GGC TCA CTG CAA CCT CTG CCT CCC GGG CTC AAG CGA TTC			1010
Pro Asn Leu Gly Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe			
320	325	330	
TCC TGT CTC AGC CTC CCA AGC AGC TGG GAT TAC GGG CAC CTG CCA CCA			1058
Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro			
335	340	345	
CAC CCC GCT AAT TTT TGT ATT TTC ATT AGA GGC GGG GTT TCA CCA TAT			1106
His Pro Ala Asn Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr			
350	355	360	
TTG TCA GGC TGG TCT CAA ACT CCT GAC CTC AGG TGACCCACCT GCCTCAGCCT			1159
Leu Ser Gly Trp Ser Gln Thr Pro Asp Leu Arg			
365	370	375	
TCCAAAGTGC TGGGATTACA GGCGTGAGCC ACCTCACCCA GCCGGCTAAT TTAGATAAAA			1219
AAATATGTAG CAATGGGGGG TCTTGCTATG TTGCCAGGC TGGTCTCAAA CTTCTGGCTT			1279
CATGCAATCC TTCCAAATGA GCCACAAACAC CCAGCCAGTC ACATTTTTAACAGTTACA			1339
TCTTTATTTAGTACTAG AAAGTAATAC AATAAACATG TCAAACCTGC AAATTCAGTA			1399
GTAACAGAGT TCTTTATAA CTTTAAACA AAGCTTTAGA GCA			1442

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Glu	Phe	Ser	Leu	Leu	Leu	Pro	Arg	Leu	Glu	Cys	Asn	Gly	Ala	Ile
1				5					10					15	

Ser	Ala	His	Arg	Asn	Leu	Arg	Leu	Pro	Gly	Ser	Ser	Asp	Ser	Pro	Ala
					20			25				30			

Ser	Ala	Ser	Pro	Val	Ala	Gly	Ile	Thr	Gly	Met	Cys	Thr	His	Ala	Arg
					35			40			45				

Leu	Ile	Leu	Tyr	Phe	Phe	Leu	Val	Glu	Met	Glu	Phe	Leu	His	Val	Gly
						50		55			60				

Gln	Ala	Gly	Leu	Glu	Leu	Pro	Thr	Ser	Asp	Asp	Pro	Ser	Val	Ser	Ala
						65		70			75		80		

Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala Arg Leu Cys Leu

85

90

95

Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met Cys Pro Ser Trp
 100 105 110

Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu Pro Lys Cys Trp
 115 120 125

Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile Leu Phe Phe Leu
 130 135 140

Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val Gln Trp Cys Asp
 145 150 155 160

His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys His Pro Pro Ala
 165 170 175

Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His His Tyr Thr Trp
 180 185 190

Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln Ser Leu Asn Ser
 195 200 205

Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly Ser Leu Gln Pro
 210 215 220

Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser Leu Leu Ser Ser
 225 230 235 240

Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe Phe Val Phe Leu
 245 250 255

Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile Leu Ile Ser Gly
 260 265 270

Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala Gly Ile Thr Gly
 275 280 285

Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys Leu Phe Glu Met
 290 295 300

Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp Pro Asn Leu Gly
 305 310 315 320

Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe Ser Cys Leu Ser
 325 330 335

Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro His Pro Ala Asn
 340 345 350

Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr Leu Ser Gly Trp
 355 360 365

Ser Gln Thr Pro Asp Leu Arg
 370 375

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1381 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTTTTTTTT GAGATGGAGT TTTCGCTCTT GTGCCAGG CTGGAGTGCA ATGGCGCAAT 60
CTCAGCTCAC CGAACCTCC GCCTCCGGG TTCAAGCGAT TCTCCTGCCT CAGCCTCCCC 120
AGTAGCTGGG ATTACAGGCA TGTGCACCAC GCTCGGCTAA TTTTGTATTT TTTTTTAGTA 180
GAGATGGAGT TAAACTCCAT GTGGTCAGG CTGGTCTCGA ACTCCCGACC TCAGATGATC 240
TCCCGTCTCG GCCTGCCAA AGTGTGAGA TTACAGGCAT GAGCCACCAT GCCCGGCCTC 300
TGCCTGGCTA ATTTTGTTGG TAGAACAGG GTTCACTGA TGTTGCCAA GCTGGTCTCC 360
TGAGCTCAAG CAGTCCACCT GCCTCAGCCT CCCAAAGTGC TGGGATTACA GGCGTCAGCC 420
GTGCCTGGCC TTTTATTAA ATTTTTTTA AGACACAGGT GTACCACTCT TACCCAGGAT 480
GAAGTGCAGT GGTGTGATCA CAGCTCACTG CAGCCTCAA CTCCTGAGAT CAAGCAATCC 540
TCCTGCCTCA GCCTCCCAAG TAGCTGGAC CAAAGACATG CACCACTACA CCTGGTAATT 600
TTTATTAA TTTTAATTT TTTGAGACAG AGTCTCACTC TGTCACCCAG GCTGGAGTGC 660
AGTGGCGCAA TCTGGCTCA CTGCAACCTC TGCTCCGG GTCAAGTTA TTCTCCTGCC 720
CCAGCCTCCT GAGTAGCTGG GACTACAGGC GCCCACCACG CCTAGCTAAT TTTTTGTAT 780
TTTTAGTAGA GATGGGGTTT CACCATGTTG GCCAGGTTGA TCTTGATCTC TTGACCTTGT 840
GATCTGCCTG CCTCGGCCTA CCCAAAGTGC TGGGATTACA GGCGTGACT CCACGCCGGC 900
CTATTTAA TTTTGTTTG TTTGAAATGG AATCTCACTC TGTTACCCAG GTCGGAGTGC 960
AATGGCAAAT CTCGGCTACT CGAACCTCT GCCTCCGGG TCAAGCGATT CTCCGTCTC 1020
AGCCTCCAA GCAGCTGGGA TTACGGGACC TGCACCACAC CCCGCTAATT TTTGTATTT 1080
CATTAGAGGC GGGTTACCA TATTGTCAG GCTGGGTCTC AAACCTCTGA CCTCAGGTGA 1140
CCCACCTGCC TCAGCCTTCC AAAGTGTGG GATTACAGGC GTGAGCCACC TCACCCAGCC 1200
GGCTAATTG GAATAAAAAA TATGTAGCAA TGGGGGTCTG CTATGTTGCC CAGGCTGGTC 1260
TCAAACCTCT GGCTTCAGTC AATCCTTCCA AATGAGCCAC AACACCCAGC CAGTCACATT 1320
TTTTAAACAG TTACATCTT ATTGAGTAT ACTAGAAAGT AATACAATAA ACATGTCAA 1380
C 1381

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTTTTTTTT GAGATGGAGT TTTCGCTCTT GTGCCAGG CTGGAGTGCA ATGGCGCAAT 60
CTCAGCTCAC CGCAACCTCC GCCTCCCCGG TTCAAGCGAT TCTCCTGCCT CAGCCTCCCC 120
AGTAGGCTGG GATTACAGGC ATGTGCACCA CGCTCGGCTA ATTTTGTATT TTTTTTTAGT 180
AGAGATGGAG TTTCTCCATG TTGGTCAGGC TGGTCTCGAA CTCCGACCTC AGATGATCCT 240
CCCGTCTCGG CCTCCCAAAG TGCTAGATAAC AGGACTGAGC ACCATGCCCG GCCTCTGCCT 300
GGCTAATTT TGTGGTAGAA ACAGGGTTTC ACTGATGTGC CCAAGCTGGT CTCCTGAGCT 360
CAAGCAGTCC ACCTGCCTCA GCCTCCCCAA GTGCTGGGAT TACAGGCGTG CAGCCGTGCC 420
TGGCCTTTT ATTTTATTTT TTTTAAGACA CAGGTGTCCC ACTCTTACCC AGGATGAAGT 480
GCAGTGGTGT GATCACAGCT CACTGCAGCC TTCAACTCTG AGATCAAGCA TCCTCCTGCC 540
TCAGCCTCCC AAAGTAGCTG GGACCAAAGA CATGCACCAC TACACCTGGC TAATTTTAT 600
TTTTATTTT AATTTTTGA GACAGAGTCT CAACTCTGTC ACCCAGGCTG GAGTGCAGTG 660
GCGCAATCTT GGCTCACTGC AACCTCTGCC TCCCGGGTTC AAGTTATTCT CCTGCCAG 720
CCTCCTGAGT AGCTGGGACT ACAGGCGCCC ACCACGCCTA GCTAATTTT TTGTATTTT 780
AGTAGAGATG GGGTTTCACC ATGTTGCCA GGTTGATGCT AGATCTCTT ACCTTGTGAT 840
CTGCCTGCC CGGCCTCCC AAGTGTGGG ATTACAGGAC GTGACGCCA CGGCCGGCC 900
TATTTTTAAT TTTGTGTGT TTGAAATGGA ATCTCACTCT GTTACCCAGG CTGGAGTGCA 960
ATGGCAAAT CTCGGCTCAC TGCAACCTCT GCCTCCCGGG CTCAAGCGAT TCTCCTGTCT 1020
CAGCCTCCC AGCAGCTGGG ATTACGGCA CCTGCACCAC ACCCGCTAA TTTTGTATT 1080
TTCATTAGAG GCGGGGTTTC ACCATATTTG TCAGGCTGGT CTCAAACTCC TGACCTCAGG 1140
TGACCCACCT GCCTCAGCCT TCCAAAGTGC TGGGATTACA GGCAGTGACGC CTCACCCAGC 1200
CGGCTAATT AGATAAAAAA ATATGTAGCA ATGGGGGGTC TTGCTATGTT GCCCAGGCTG 1260
GTCTCAAAC TCTGGCTTCA TGCAATCCTT CCAAATGAGC CACAACACCC AGCCAGTCAC 1320
ATTTTTAAC AGTTACATCT TTATTTAGT ATACTAGAAA GTGATACGAT AACATGGCGG 1380
AACCTGCAA TTCGAGTAGT ACAGAGTCTT TTATAACT 1418

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGTCCCCACTC TTACCCAGGA TG

22

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AAGCAGGCAG ATCACAAAGGT CCAG

24

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AATGGATGAC GATATCGCTG

20

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGAGGTAGT CTGTCAGGT

19

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTCATCCTGG GTAAGAGTGG GACACCTGTG

30

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGGTGCATGT CTTGGTCCC AGCTAC

26

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATCAACCTGG CGAACATGGT GAACCCCATC

30

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CACTGCAC TT NCCA

14

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

00964528-0092804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCAGGTGTAG NCCA

14

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CAAGGTCCAG NCCA

14

0964628 - DECODED